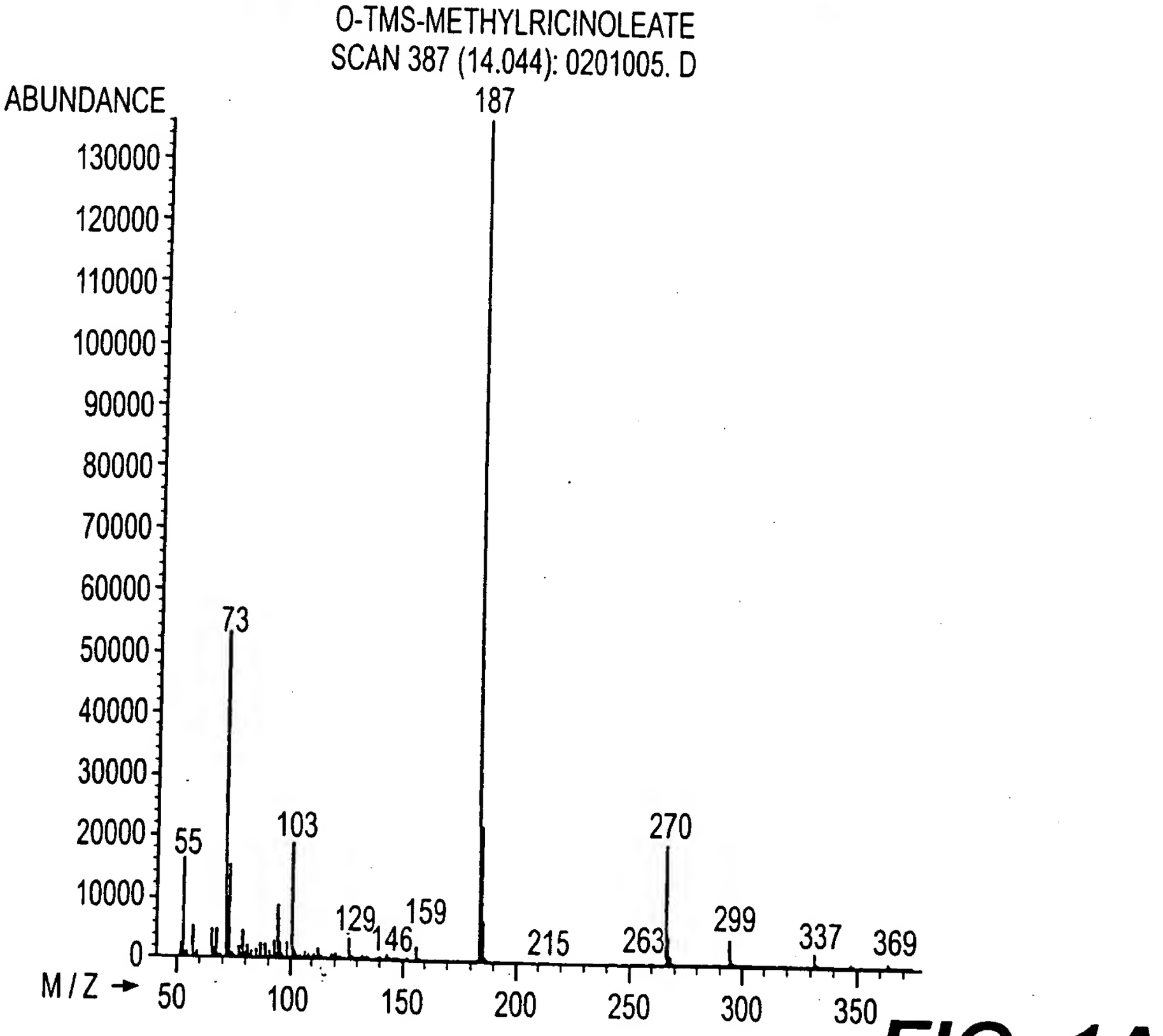

O-TMS-METHYLRICINOLEATE
SCAN 387 (14.044): 0201005. D
ABUNDANCE
187
130000
120000
110000
100000
90000
80000
70000
60000
50000
40000
30000
20000
10000
0
73
55
103
129
146
159
215
263
270
299
337
369
M/Z →
50
100
150
200
250
300
350

FIG. 1A

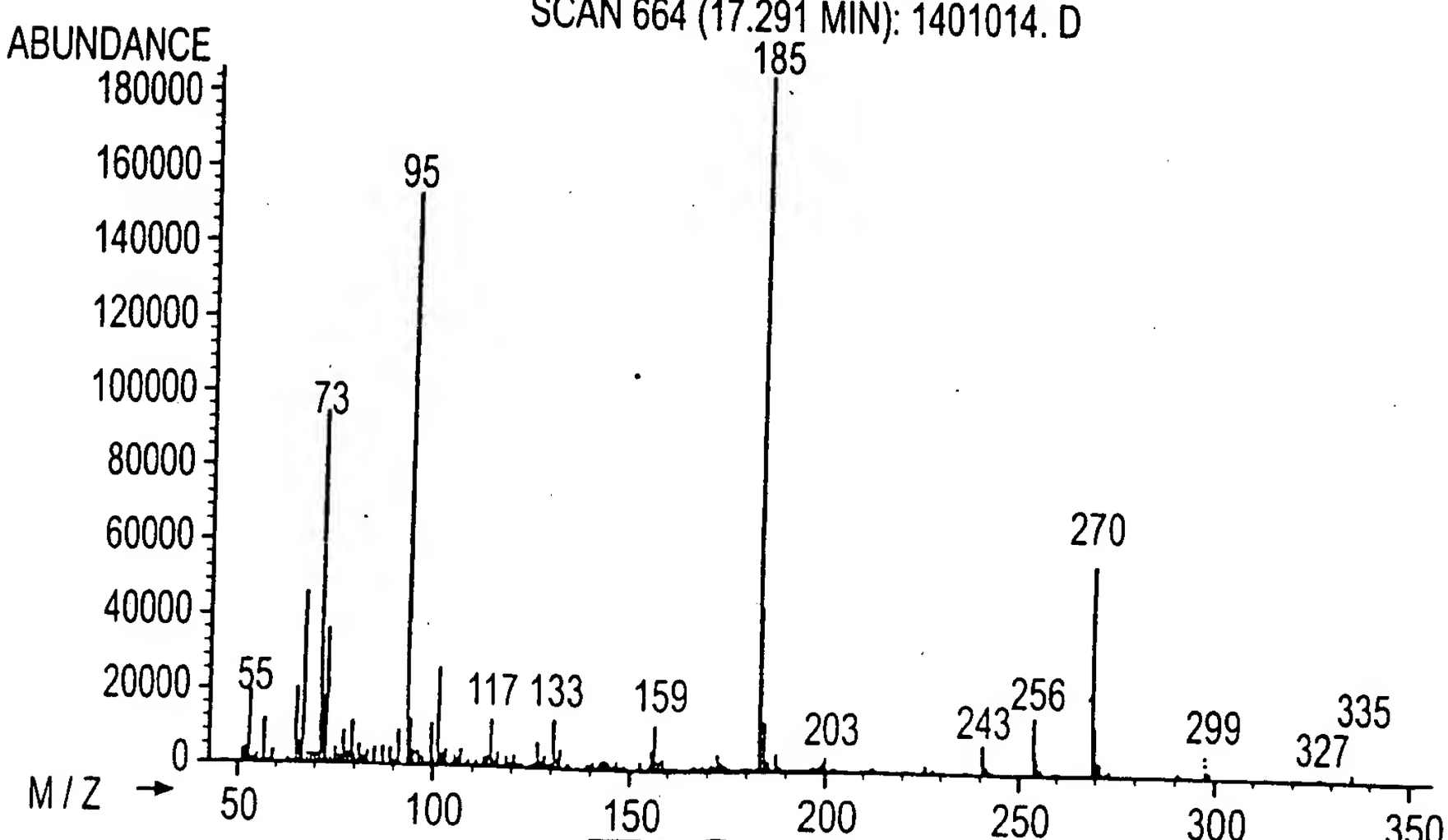

O-TMS-METHYLDENSIPOLEATE
SCAN 664 (17.291 MIN): 1401014. D
ABUNDANCE
185
180000
160000
140000
120000
100000
80000
60000
40000
20000
0
95
73
55
117
133
159
203
243
256
270
299
327
335
M/Z →
50
100
150
200
250
300
350

FIG. 1B

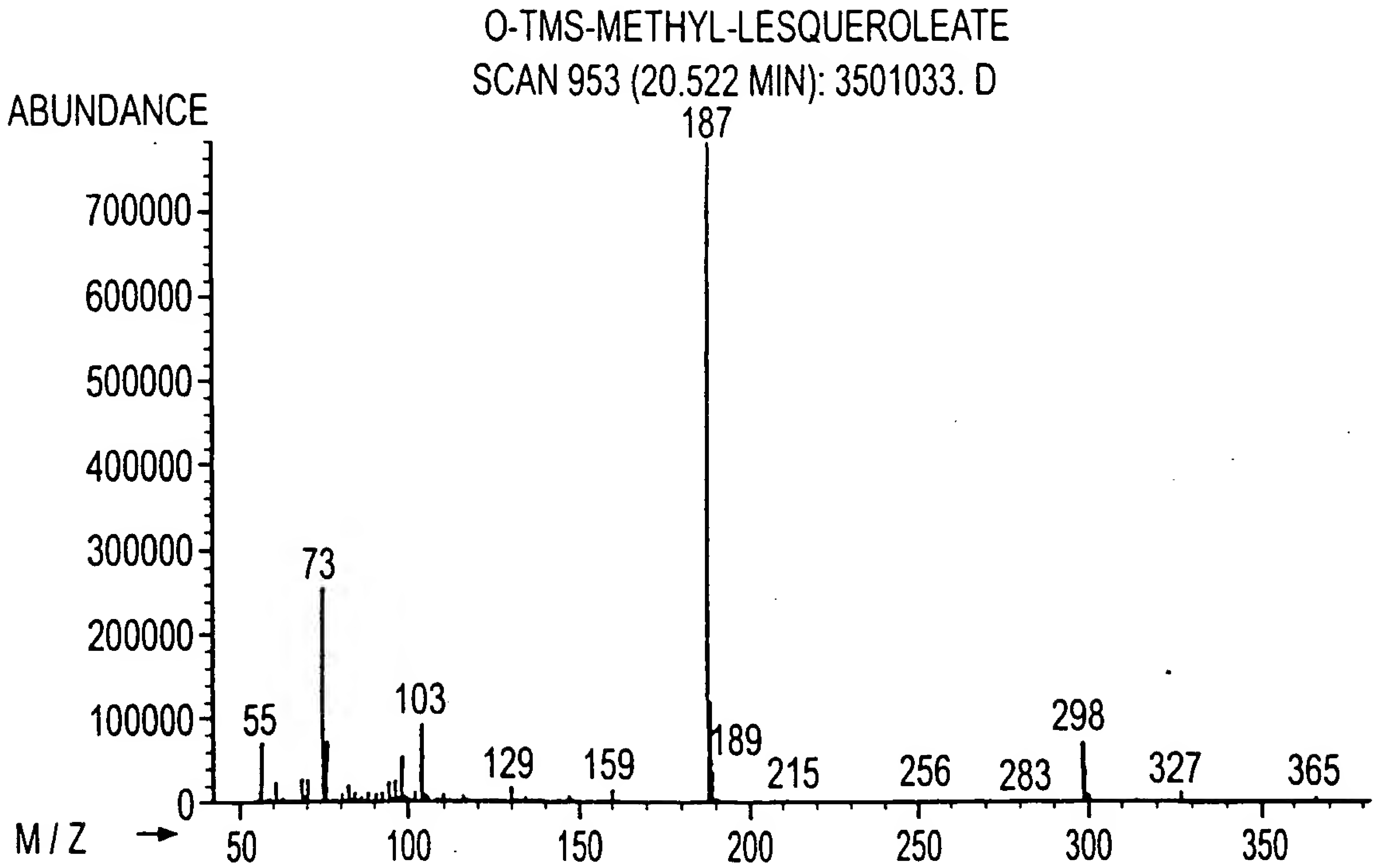

O-TMS-METHYL-LESQUEROLEATE
SCAN 953 (20.522 MIN): 3501033. D
ABUNDANCE
700000
600000
500000
400000
300000
200000
100000
0
187
73
55
103
129
159
189
215
256
283
298
327
365
M / Z
50
100
150
200
250
300
350

FIG. 1C

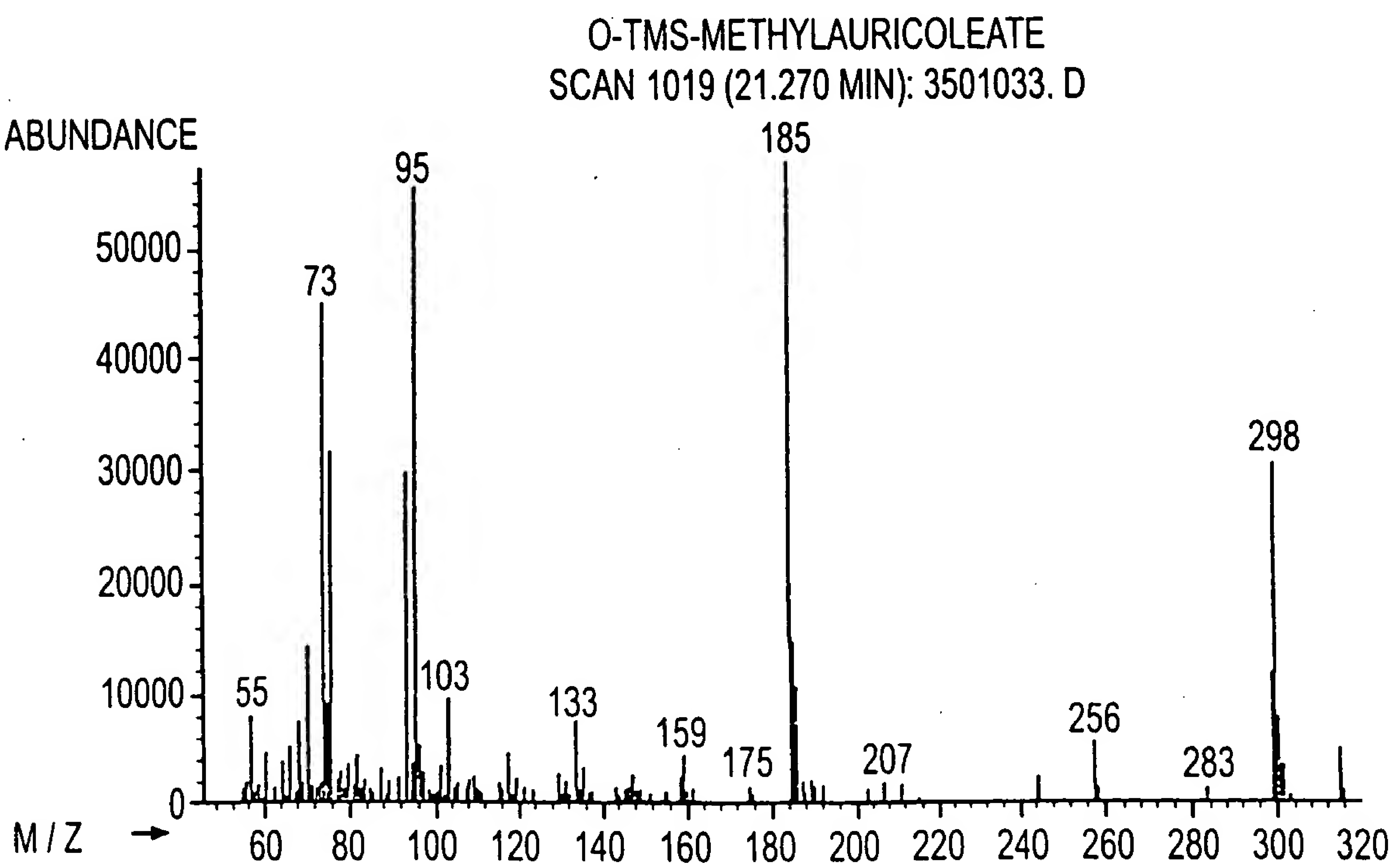
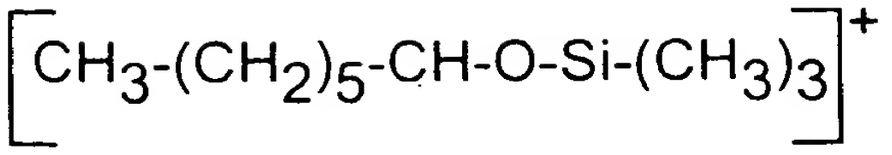
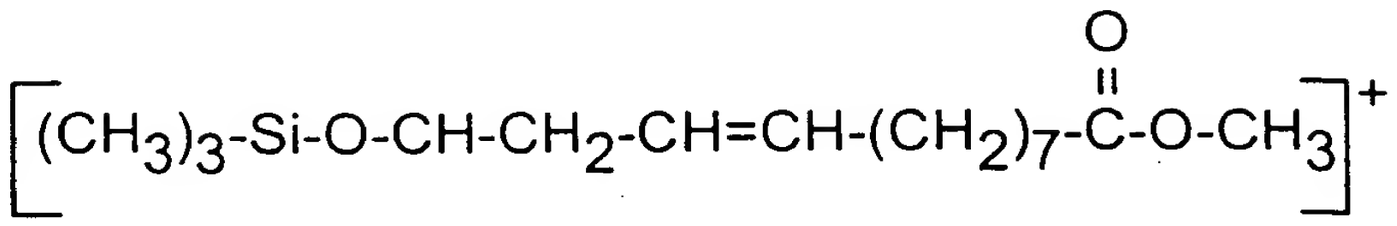

O-TMS-METHYLAURICOLEATE
SCAN 1019 (21.270 MIN): 3501033. D
ABUNDANCE
50000
40000
30000
20000
10000
0
185
95
73
298
55
103
133
159
175
207
256
283
M / Z
60
80
100
120
140
160
180
200
220
240
260
280
300
320

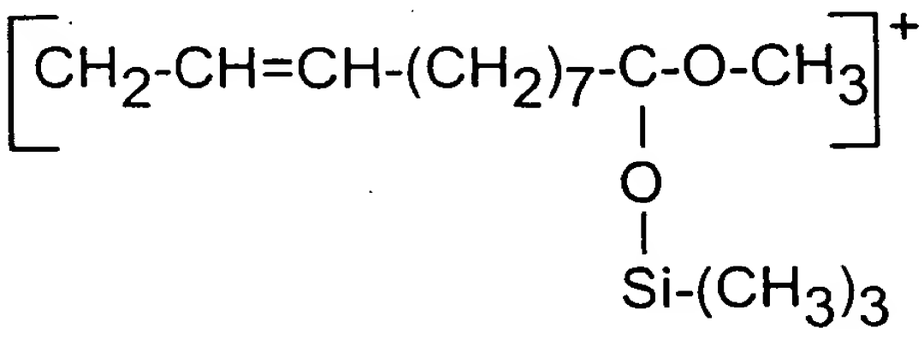
FIG. 1D

LON #1: MASS 187 

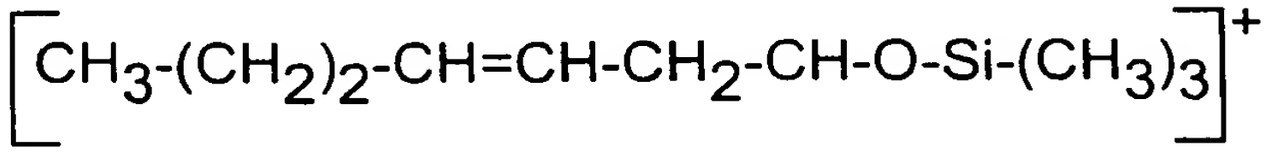
LON #2: MASS 299



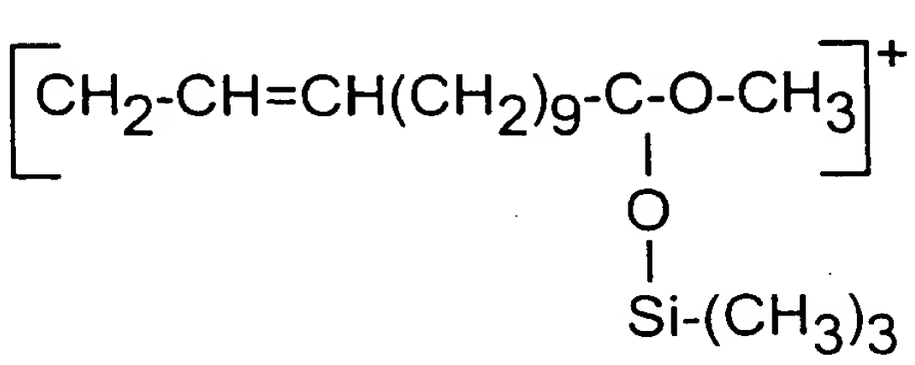
LON #3: MASS 270 (CHARACTERISTIC REARRANGEMENT ION)



LON #4: MASS 185 (DESATURATED ANALOG OF LON #1)



LON #5: MASS 298 (ELONGATED ANALOG OF LON #3)



LON #6: MASS 327 (ELONGATED ANALOG OF ION)

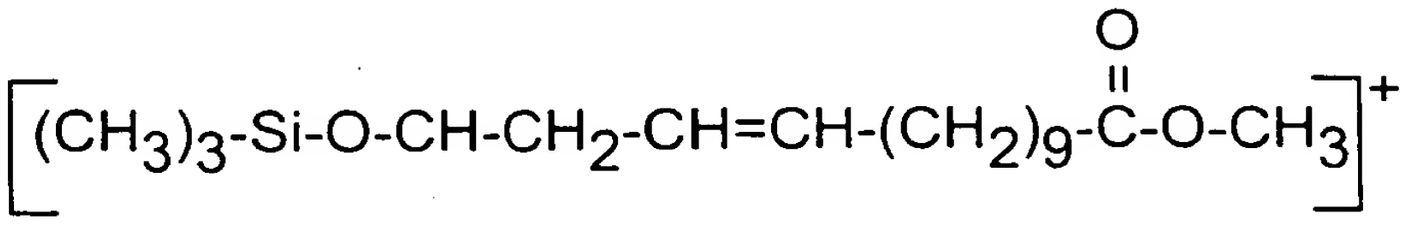


FIG. 2

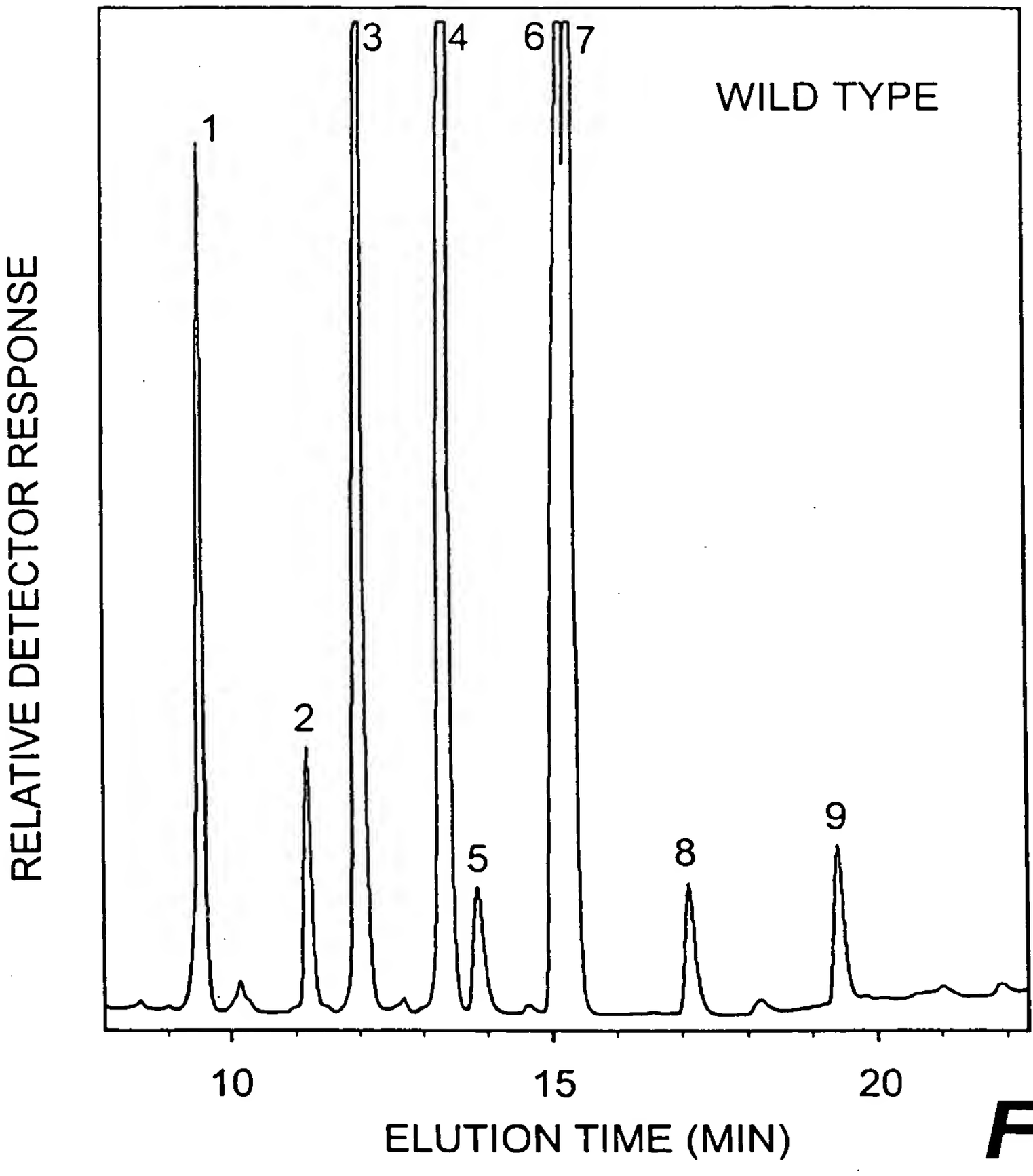

WILD TYPE
RELATIVE DETECTOR RESPONSE
1
2
3
4
5
6
7
8
9
10
15
20
ELUTION TIME (MIN)

FIG. 3A

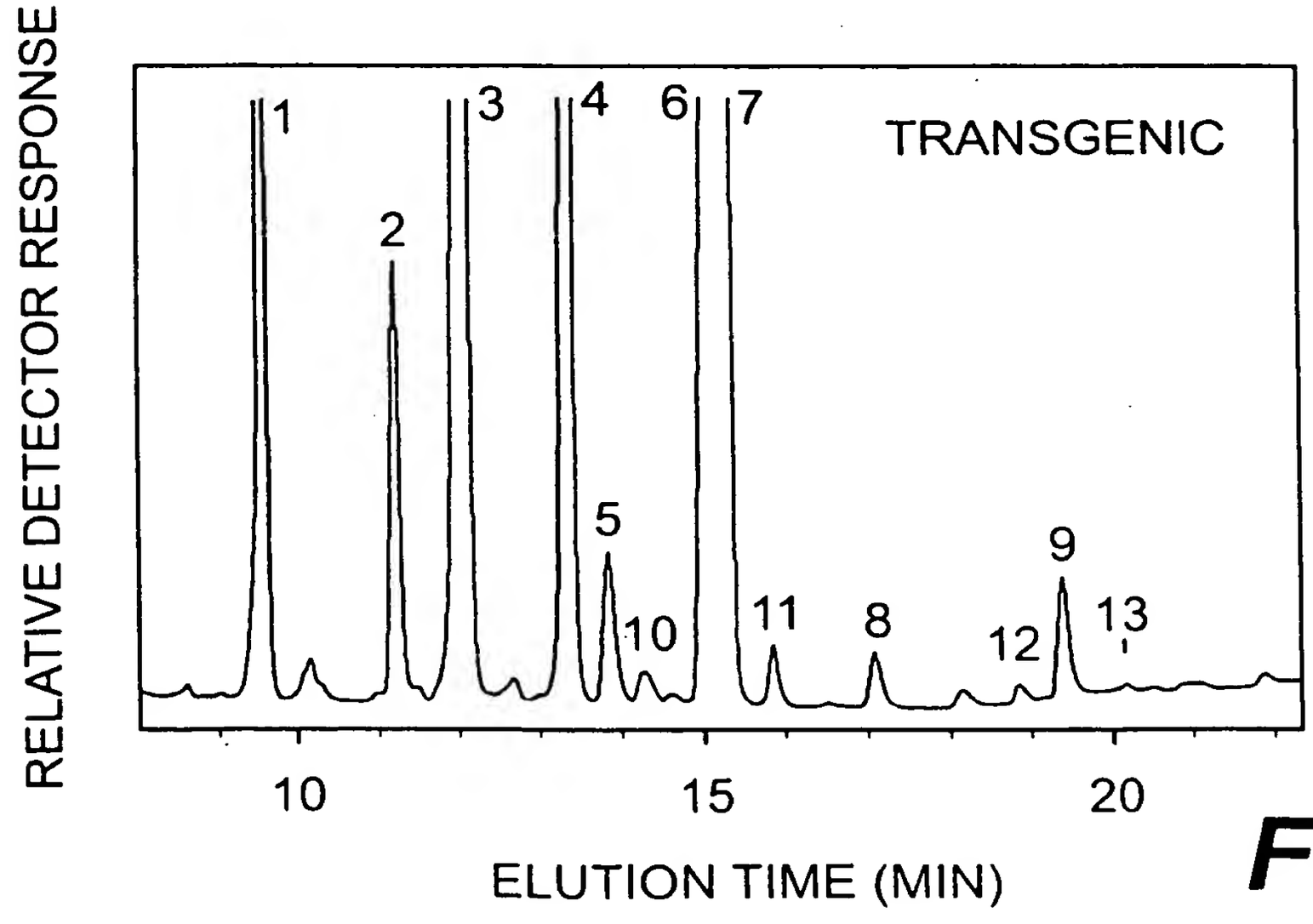

TRANSGENIC
RELATIVE DETECTOR RESPONSE
1
2
3
4
5
6
7
8
9
10
11
12
13
10
15
20
ELUTION TIME (MIN)

FIG. 3B

MASS SPECTRUM OF PEAK 10 FROM FIGURE 3B
SCAN 485 (15.203 MIN): 1501001. D

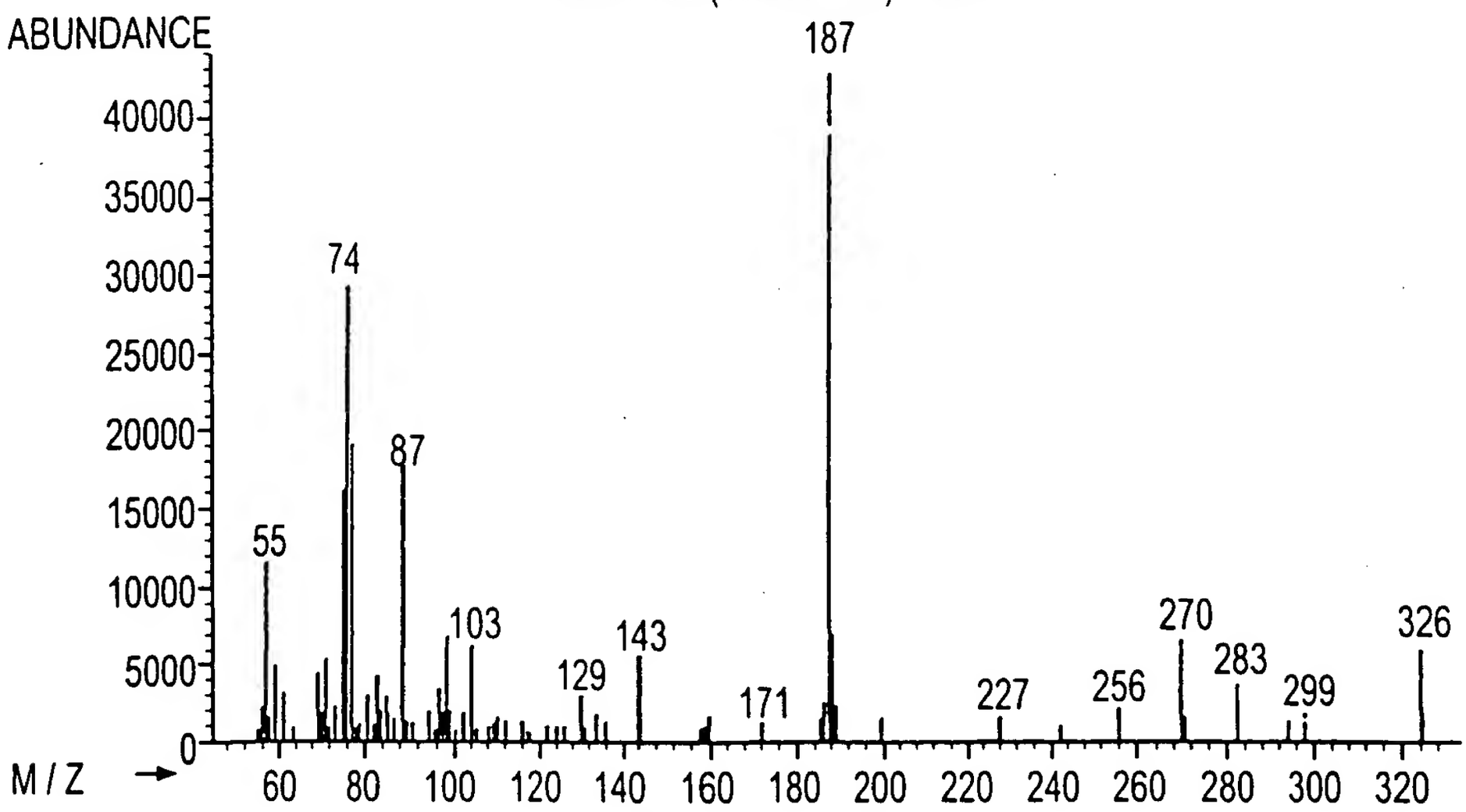


FIG. 4A

MASS SPECTRUM OF PEAK 11 FROM FIGURE 3B

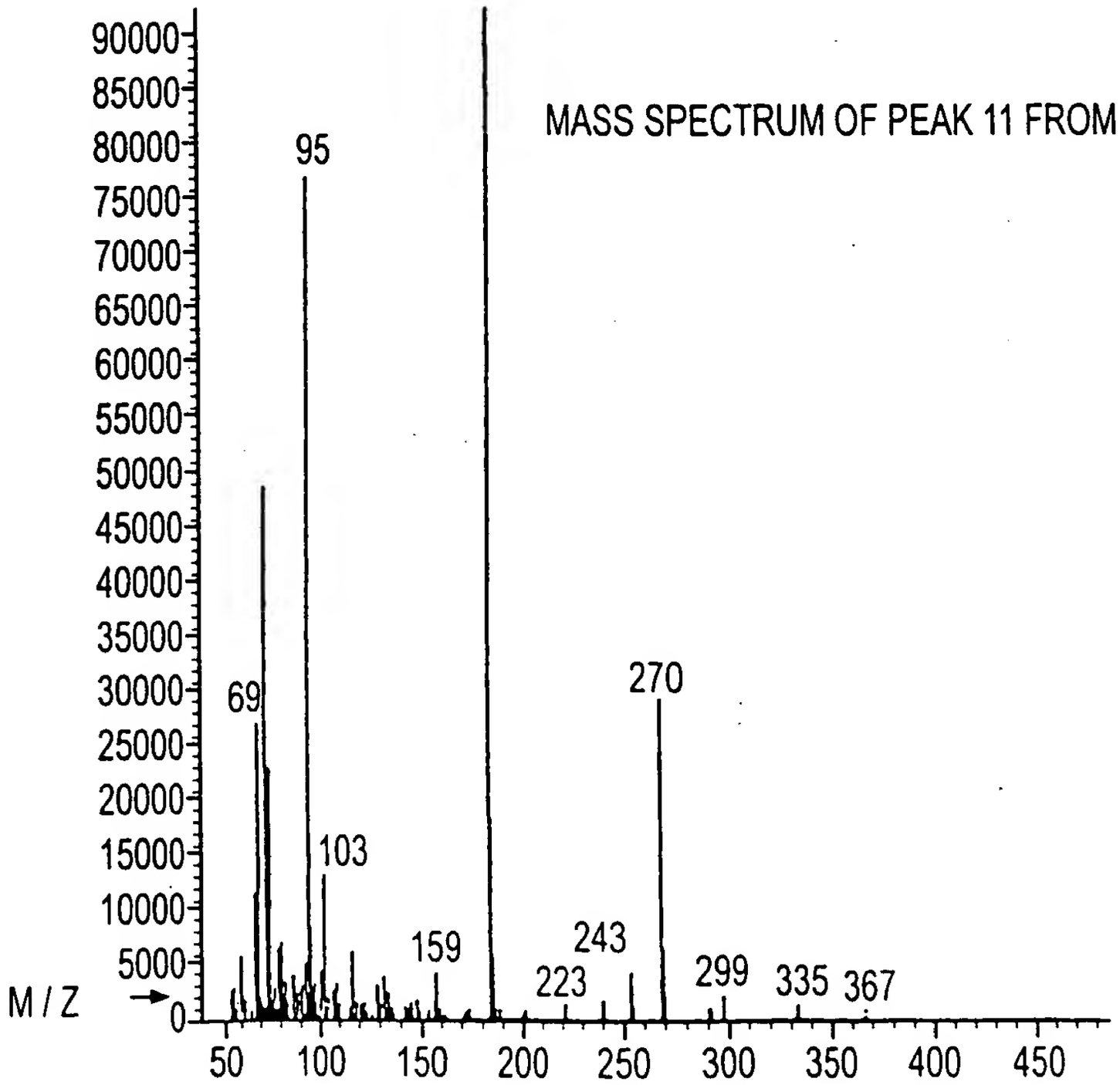


FIG. 4B

MASS SPECTRUM OF PEAK 12 FROM FIGURE 3B
SCAN 806 (18.825 MIN): 1401017. D

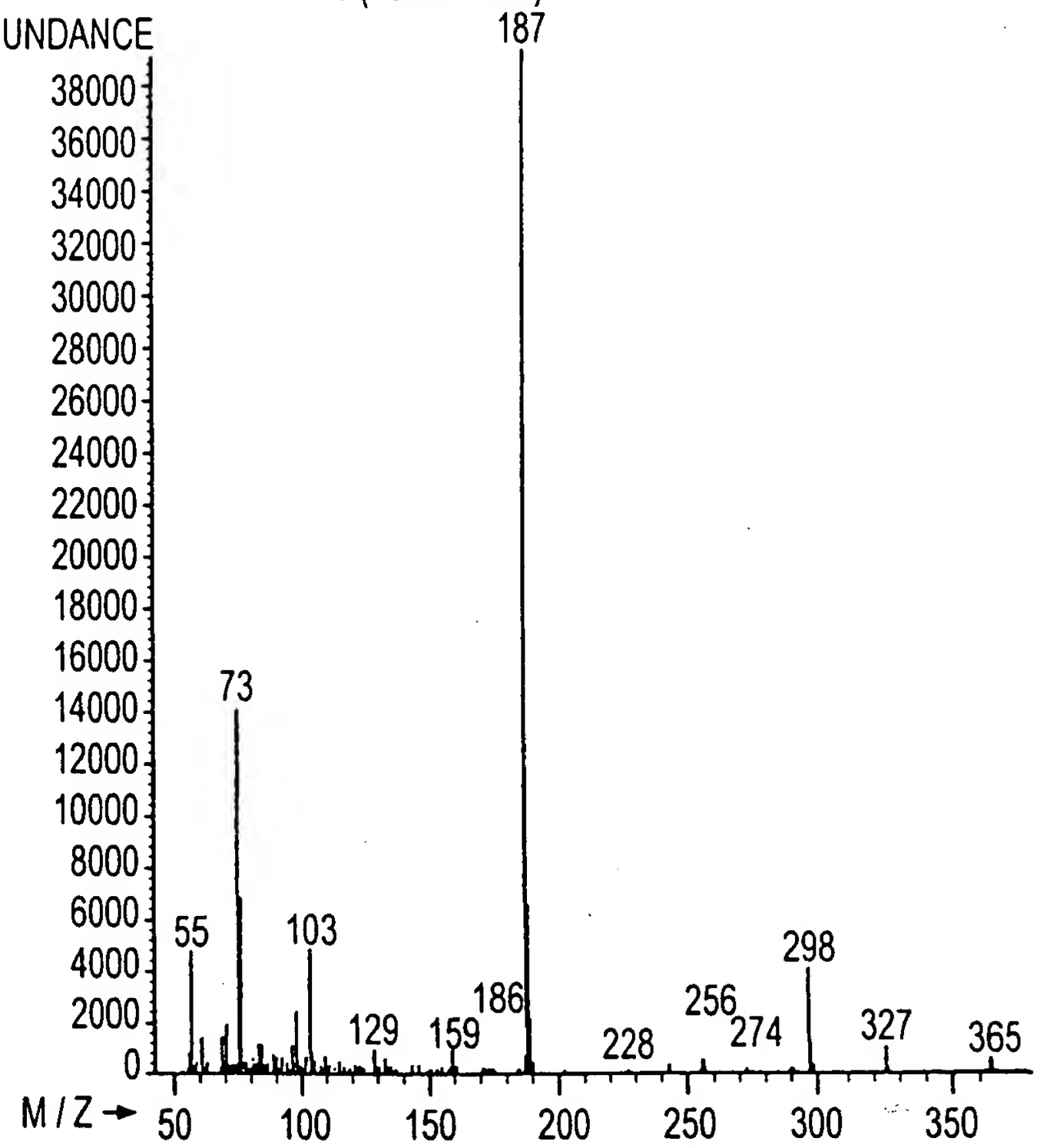


FIG. 4C

MASS SPECTRUM OF PEAK 13 FROM FIGURE 3B
SCAN 997 (20.974 MIN): 1501001. D

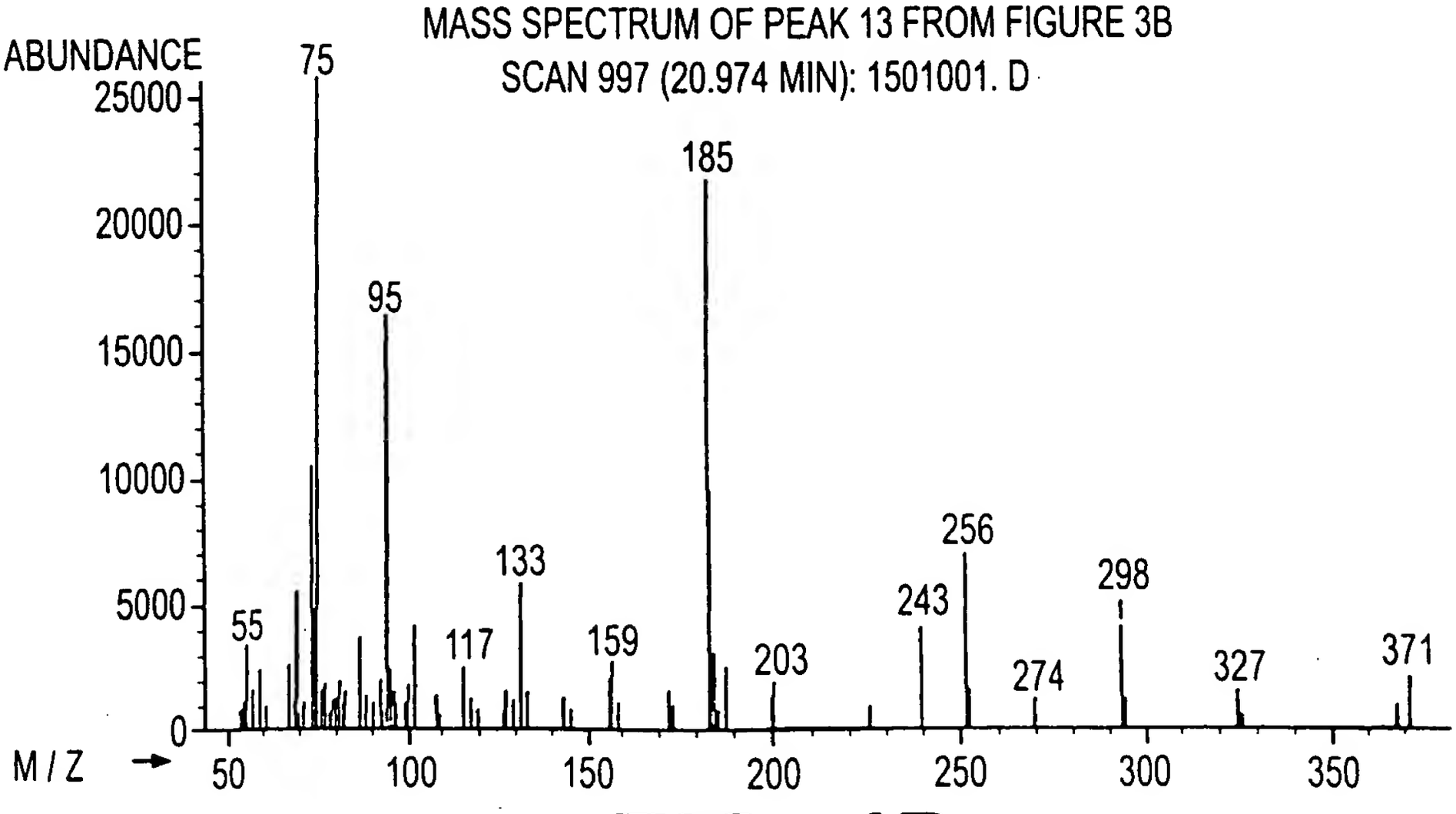


FIG. 4D

10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACTTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					
CAC					

FIG. 5

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAATACC	TCAACAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAACTGTCCA	GTTCGTCCTC	GGATGGCCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAAC
250	260	270	280	290	300
GACCGTGAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCTGCG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCATC	AGAGTGGGAT	TGGCTTAGAG	GAGCTTTAGC	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTC	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					
CACT					

FIG. 6

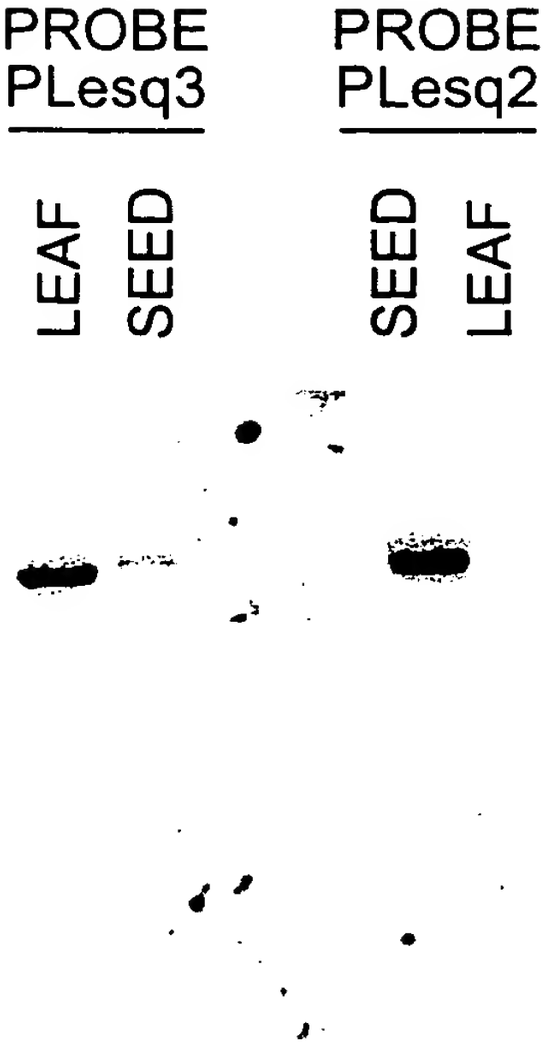


FIG. 7

```
 AT  GAA  GCT  TTA  TAA  GAA  GTT  AGT  TTT  CTC  TGG  TGA  CAG  AGA  AAT  TNT      47

GCT  AAT  TGG  TAG  TGA  CAG  TTG  AAG  CAA  CAG  GAA  CAA  CAA  GGA  TGG  TTG      95

GTG  NTG  ATG  CTG  ATG  TGG  TGA  TGT  GTT  ATT  CAT  CAA  ATA  CTA  AAT  ACT     143

ACA  TTA  CTT  GTT  GCT  GCC  TAC  TTC  TCC  TAT  TTC  CTC  CGC  CAC  CCA  TTT     191

TGG  ACC  CAC  GAN  CCT  TCC  ATT  TAA  ACC  CTC  TCT  CGT  GCT  ATT  CAC  CAG     239

AAG  AGA  AGC  CAA  GAG  AGA  GAG  AGA  GAG  AAT  GTT  CTG  AGG  ATC  ATT  GTC     287

TTC  TTC  ATC  GTT  ATT  AAC  GTA  AGT  TTT  TTT  TGA  CCA  CTC  ATA  TCT  AAA     335

ATC  TAG  TAC  ATG  CAA  TAG  ATT  AAT  GAC  TGT  TCC  TTC  TTT  TGA  TAT  TTT     383

                         Met  Gly  Ala  Gly  Gly  Arg  Ile  Met  Val  Thr      10
CAG  CTT  CTT  GAA  TTC  AAG  ATG  GGT  GCT  GGT  GGA  AGA  ATA  ATG  GTT  ACC     431

Pro  Ser  Ser  Lys  Lys  Ser  Glu  Thr  Glu  Ala  Leu  Lys  Arg  Gly  Pro  Cys      26
CCC  TCT  TCC  AAG  AAA  TCA  GAA  ACT  GAA  GCC  CTA  AAA  CGT  GGA  CCA  TGT     479

Glu  Lys  Pro  Pro  Phe  Thr  Val  Lys  Asp  Leu  Lys  Lys  Ala  ILe  Pro  Gln      42
GAG  AAA  CCA  CCA  TTC  ACT  GTT  AAA  GAT  CTG  AAG  AAA  GCA  ATC  CCA  CAG     527
```

FIG. 8A (CONT-1)

His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	58
CAT	TGT	TTC	AAG	CGC	TCT	ATC	CCT	CGT	TCT	TTC	TCC	TAC	CTT	CTC	ACA	575
Asp	Ile	Thr	Leu	Val	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	74
GAT	ATC	ACT	TTA	GTT	TCT	TGC	TTC	TAC	TAC	GTT	GCC	ACA	AAT	TAC	TTC	623
Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	90
TCT	CTT	CTT	CCT	CAG	CCT	CTC	TCT	ACT	TAC	CTA	GCT	TGG	CCT	CTC	TAT	671
Trp	Val	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	106
TGG	GTA	TGT	CAA	GGC	TGT	GTC	TTA	ACC	GGT	ATC	TGG	GTC	ATT	GGC	CAT	719
Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	122
GAA	TGT	GGT	CAC	CAT	GCA	TTC	AGT	GAC	TAT	CAA	TGG	GTA	GAT	GAC	ACT	767
Val	Gly	Phe	Ile	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	138
GTT	GGT	TTT	ATC	TTC	CAT	TCC	TTC	CTT	CTC	GTC	CCT	TAC	TTC	TCC	TGG	815
Lys	Tyr	Ser	His	Arg	Arg	His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	154
AAA	TAC	AGT	CAT	CGT	CGT	CAC	CAT	TCC	AAC	AAT	GGA	TCT	CTC	GAG	AAA	863
Asp	Glu	Val	Phe	Val	Pro	Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	170
GAT	GAA	GTC	TTT	GTC	CCA	CCG	AAG	AAA	GCT	GCA	GTC	AAA	TGG	TAT	GTT	911
Lys	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	186
AAA	TAC	CTC	AAC	AAC	CCT	CTT	GGA	CGC	ATT	CTG	GTG	TTA	ACA	GTT	CAG	959

FIG. 8A (CONT-2)

Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg 202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA 1007

Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe 218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT 1055

Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu 234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA 1103

Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr 250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT 1151

Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe 266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC 1199

Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His 282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT 1247

Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val 298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA 1295

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp 314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC 1343

Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala 330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA 1391

FIG. 8B (CONT-1)

Met	Glu	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	346
ATG	GAA	GCT	ACA	GAG	GCG	ATA	AAG	CCA	ATA	CTT	GGT	GAT	TAC	TAC	CAC	1439
Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	362
TTC	GAT	GGA	ACA	CCG	TGG	TAT	GTG	GCC	ATG	TAT	AGG	GAA	GCA	AAG	GAG	1487
Cys	Leu	Tyr	Val	Glu	Pro	Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	378
TGT	CTC	TAT	GTA	GAA	CCG	GAT	ACG	GAA	CGT	GGG	AAG	AAA	GGT	GTC	TAC	1535
Tyr	Tyr	Asn	Asn	Lys	Leu											384
TAT	TAC	AAC	AAT	AAG	TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	1583
ATC	AAT	CTT	CAT	TTC	CAT	GTT	TTA	GGT	GTC	TTG	TTT	AAG	AAG	CTA	TGC	1631
TTT	GTT	TCA	ATA	ATC	TCA	GAG	TCC	ATN	TAG	TTG	TGT	TCT	GGT	GCA	TTT	1679
TGC	CTA	GTT	ATG	TGG	TGT	CGG	AAG	TTA	GTG	TTC	AAA	CTG	CTT	CCT	GCT	1727
GTG	CTG	CCC	AGT	GAA	GAA	CAA	GTT	TAC	GTG	TTT	AAA	ATA	CTC	GGA	ACG	1775
AAT	TGA	CCA	CAA	NAT	ATC	CAA	AAC	CGG	CTA	TCC	GAA	TTC	CAT	ATC	CGA	1823
AAA	CCG	GAT	ATC	CAA	ATT	TCC	AGA	GTA	CTT	AG						1855

FIG. 8B (CONT-2)

		10	20	30	40	50	
LFFAH12	1	MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50
FAH12	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKRAIPPHC	50
ATFAD2	1	MGAGGRMP--	--VPTSSKKS	--ETDTTKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2	1	MGAGGRMQ--	--VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1	1	MGLA-KETTM	GGRGRVAKVE	VQGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50
GMFAD2-2	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSLS	QIKKAIPPHC	50
ZMFAD2	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC	50
RCFAD2	1	----------	----------	----------	----------	----------	50
		60	70	80	90	100	
LFFAH12	51	FKRSIPRSFS	YLLTDITLVS	CFYYVATNYF	SLLPQPLSTY	LAWPLYWVCQ	100
FAH12	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVYWLFQ	100
ATFAD2	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	LAWPLYWACQ	100
BNFAD2	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAWPLYWACQ	100
GMFAD2-1	51	FQRSLLTSFS	YVVYDLSFAF	IFY-IATTYF	HLLPQPFS-L	IAWPIYWVLQ	100
GMFAD2-2	51	FQRSVLRSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	RGMAIYWAVQ	100
ZMFAD2	51	FERSVLKSFS	YVVHDLVIAA	ALLYFALAII	PALPSPLR-Y	AAWPLYWIAQ	100
RCFAD2	1	----------	----------	----------	----------	----------	100
		110	120	130	140	150	
LFFAH12	101	GCVLTGIWVI	GHECGHHAFS	DYQWVDDTVG	FIFHSFLLVP	YFSWKYSHRR	150
FAH12	101	GCILTGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR	150
ATFAD2	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
BNFAD2	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150
GMFAD2-1	101	GCLLTGVWVI	AHECGHHAFS	KYQWVDDVVG	LTLHSTLLVP	YFSWKISHRR	150
GMFAD2-2	101	GCILTGVWVI	AHECGHHAFS	DYQLLDDIVG	LILHSALLVP	YFSWKYSHRR	150
ZMFAD2	101	G---------	-------AFS	DYSLLDDVVG	LVLHSSLMVP	YFSWKYSHRR	150
RCFAD2	101	-------WVM	AHDCGHHAFS	DYQLLDDVVG	LILHSCLLVP	YFSWKHSHRR	150

FIG. 9A (CONT-1)

		160	170	180	190	200	
LFFAH12	151	HHSNNGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL	200
FAH12	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLTL	AATLLLGWPL	200
ATFAD2	151	HHSNTGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL	200
BNFAD2	151	HHSNTGSLER	DEVFVPR-RS	QTSSGTAST-	STTFGRTVML	TVQFTLGWPL	200
GMFAD2-1	151	HHSNTGSLDR	DEVFVPKPKS	KVAWFSKYL-	NNPLGRAVSL	LVTLTIGWPM	200
GMFAD2-2	151	HHSNTGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLTL	AVTLTLGWPL	200
ZMFAD2	151	HHSNTGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL	200
RCFAD2	151	HHSNTGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL	200
		210	220	230	240	250	
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR	250
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFVLYQ	250
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCFGLYR	250
BNFAD2	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP	250
GMFAD2-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR	250
GMFAD2-2	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAVVYGLFR	250
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK	250
RCFAD2	201	YLAFNVSGRP	YPR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAVTFGLYQ	250

FIG. 9A (CONT-2)

```
                          260         270         280         290         300
LFFAH12     251   YAASQGLTAM  ICVYGVPLLI  VNFFLVLVTF  LQHTHPSLPH  YDSTEWEWIR     300
FAH12       251   ATMAKGLAWV  MRIYGVPLLI  VNCFLVMITY  LQHTHPAIPR  YGSSEWDWLR     300
ATFAD2      251   YAAAQGMASM  ICLYGVPLLI  VNAFLVLITY  LQHTHPSLPH  YDSSEWDWLR     300
BNFAD2      251   YAAVQGVASM  VCFLRVPLLI  VNGFLVLITY  LQHTHPSLPH  YDSSEWDWLR     300
GMFAD2-1    251   VATLKGLVWL  LCVYGVPLLI  VNGFLVTITY  LQHTHFALPH  YDSSEWDWLK     300
GMFAD2-2    251   LAMAKGLAWV  VCVYGVPLLV  VNGFLVLITF  LQHTHPALPH  YTSSEWDWLR     300
ZMFAD2      251   LAAAFGVWWV  VRVYAVPLLI  VNAWLVLITY  LQHTHPSLPH  YDSSEWDWLR     300
RCFAD2      251   LAIAKGLAWV  VCVYGVPLLV  VNSFLVLITF  LQHTHPALPH  YDSSEWDWLR     300

                          310         320         330         340         350
LFFAH12     301   GALVTVDRDY  GILNKVFHNI  TDTHVAHHLF  ATIPHYNAME  ATEAIKPILG     350
FAH12       301   GAMVTVDRDY  GVLNKVFHNI  ADTHVAHHLF  ATVPHYHAME  ATKAIKPIMG     350
ATFAD2      301   GALATVDRDY  GILNKVFHNI  TDTHVAHHLF  STMPHYNAME  ATKAIKPILG     350
BNFAD2      301   GALATVDRDY  GILNQGFHNI  TDTHEAHHLF  STMPHYHAME  ATKAIKPILG     350
GMFAD2-1    301   GALATMDRDY  GILNKVFHHI  TDTHVAHHLF  STMPHYHAME  ATNAIKPILG     350
GMFAD2-2    301   GALATVDRDY  GILNKVFHNI  TDTHVAHHLF  STMPHYHAME  ATKAIKPILG     350
ZMFAD2      301   GALATMDRDY  GILNRVFHNI  TDTHVAHHLF  STMPHYHAME  ATKAIRPILG     350
RCFAD2      301   GALATVDRDY  GILNKVFHNI  TDTQVAHHLF  ----------  ----------     350
                          360         370         380         390         400
LFFAH12     351   DYYHFDGTPW  YVAMYREAKE  CLYVEPDTER  GKKGVYYYNN  K-L.......     400
FAH12       351   EYYRYDGTPF  YKALWREAKE  CLFVEPDEGA  PTQGVFWYRN  KY-.......     400
ATFAD2      351   DYYQFDGTPW  YVAMYREAKE  CIYVEPDREG  DKKGVYWYNN  K-L.......     400
BNFAD2      351   EYYQFDGTPV  YKAMWREAKE  CIYVEPDRQG  EKKGVFWYNN  KL*.......     400
GMFAD2-1    351   EYYQFDDTPF  YKALWREARE  CLYVEPDEGT  SEKGVYWYRN  KY*.......     400
GMFAD2-2    351   EYYRFDETPF  VKAMWREARE  CIYVEPDQST  ESKGVFWYNN  KL-.......     400
ZMFAD2      351   DYYHFDPTPV  AKATWREAGE  CIYVEPE---  DRKGVFWYNK  KF*.......     400
```

FIG. 9B

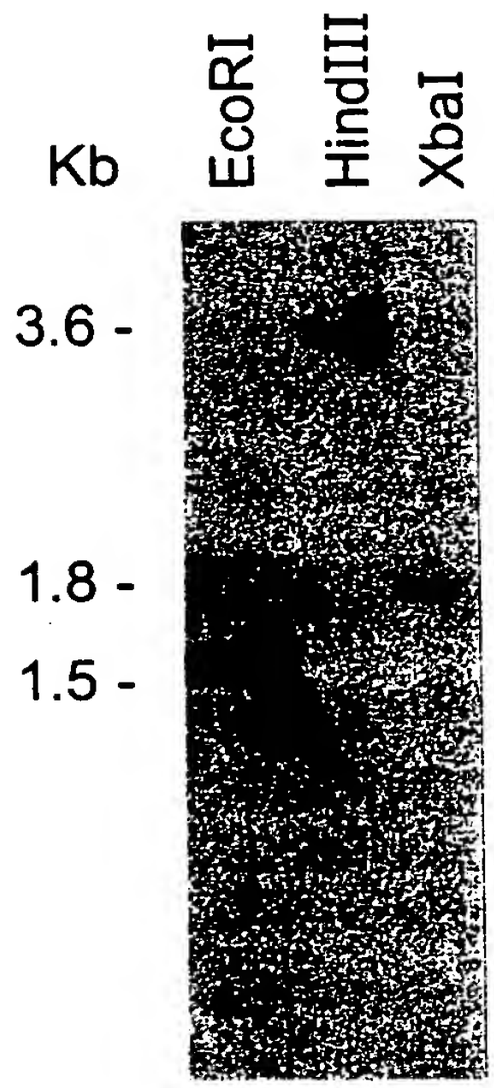


FIG. 10

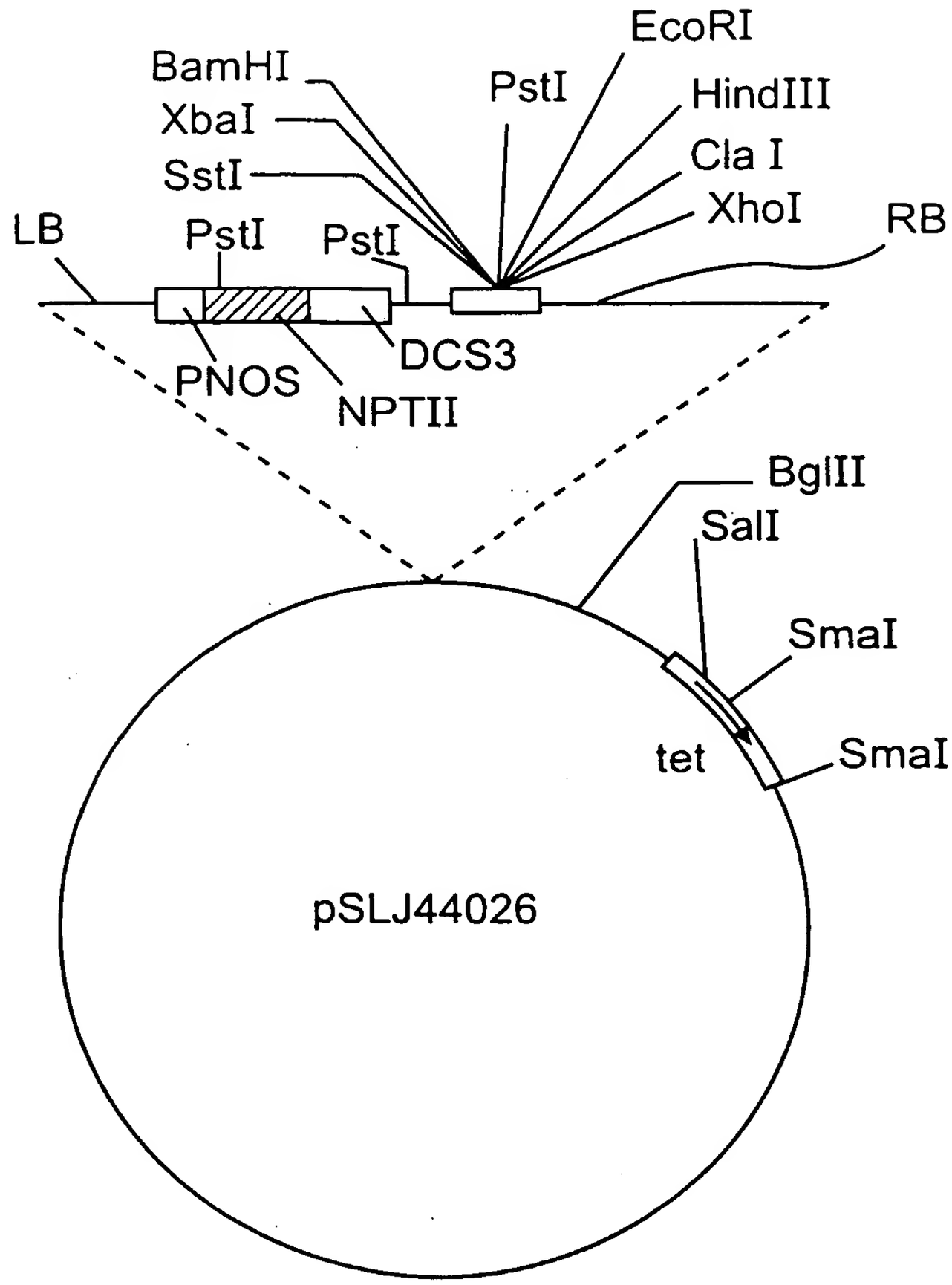

EcoRI
BamHI
PstI
HindIII
XbaI
Cla I
SstI
XhoI
RB
LB
PstI
PstI
DCS3
PNOS
NPTII
BglII
SalI
SmaI
tet
SmaI
pSLJ44026

FIG. 11